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DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Hypothetical 18.7 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RA Streusberg R.;
RT Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC018048; AAI18048.1;
DR PRINTS; PRO1641; PROMCHFAMILY.
KM Hypothetical protein.
SO SEQUENCE 165 AA; 18679 MW; 2339E8938BEC499 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1,4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLCMLGRVYRRCMV 16
DB 150 MLCMLGRVYRRCMV 165

RESULT 3
ID 09D220 PRELIMINARY; PRT; 165 AA.
AC 09D220;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE A230109K23R1k protein.
GN A230109K23R1k.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=HYPOTHALAMUS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Alakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
Schiraldi L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Oikido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Bonfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gyusztich S., Hill D., Hornann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald C., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
Hayashizaki Y.;
RT *Functional annotation of a full-length mouse cDNA collection.*;
RL Nature 409:685-690(2001).
DR EMBL; AK020723; BAB32189.1;
DR MGD; MGI:1925014; A230109K23R1k.
DR PRINTS; PRO1641; PROMCHFAMILY.
SO SEQUENCE 165 AA; 18516 MW; 1872B6B1D4BEEAC2 CRC64;

Query Match 100.0%; Score 95; DB 11; Length 165;
Best Local Similarity 100.0%; Pred. No. 1,4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MLCMLGRVYRRCMV 16
DB 150 MLCMLGRVYRRCMV 165

RESULT 4
ID 091916 PRELIMINARY; PRT; 150 AA.
AC 091916;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Melanin-concentrating hormone-like protein.
OS Paratichthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygii; Acanthopterygii; Perciformes; Pleuronectiformes;
OC Pleuronectoidae; Paratichthyidae; Paratichthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RA Jeon J., Lee J., Song Y.;
RT "Melanin-concentrating hormone-like protein."
RT Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF236090; AAF67166.1;
DR PRINTS; PRO1641; PROMCHFAMILY.
SO SEQUENCE 150 AA; 16913 MW; 117A280F46ED4499 CRC64;

Query Match 90.5%; Score 86; DB 13; Length 150;
Best Local Similarity 86.7%; Pred. No. 4,5e-07;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLCMLGRVYRRCMV 15
DB 131 MLCMLGRVYRRCMV 145

RESULT 5
ID 09B0D1 PRELIMINARY; PRT; 86 AA.
AC 09B0D1;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Pro-melanin-concentrating hormone-like 2 protein.
GN PCHL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=21108351; PubMed=11181993;
RA Counseaux A., Nelson J.L.;
RT "Birth of two chimeric genes in the Homiidae lineage."
RL Science 291:1293-1297(2001).
DR EMBL; AY008413; AAK31297.1;
DR EMBL; AY028320; AAK31290.1;
DR EMBL; AY008412; AAK31296.1;
DR PRINTS; PRO1641; PROMCHFAMILY.
SO SEQUENCE 86 AA; 9856 MW; 1C8D69B786B47471 CRC64;

Query Match 81.1%; Score 77; DB 4; Length 86;
Best Local Similarity 86.7%; Pred. No. 9,1e-06;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 LRCMLGRVYRRCMV 16
DB 72 LRCMLGRVYRRCMV 86

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Db 33 KCEYCGKVERTCQMOL 47

RESULT 8

ID DBX2X6 PRELIMINARY; PRT: 186 AA.

AC DBX2X6

DT 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Hypothetical protein ECA4988.

OS ECS4988.

GN Escherichia coli O157:H7.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI\_TaxID=83334;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / RIMD 0309952;

RX MEDLINE=21156231; PubMed=11258796;

RA Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Rida T., Takami H., Honda T., Sasakiwa C., Ogawara N., Yasunaga T., Kohara S., Shibata T., Hatiori M., Shinagawa H. ;

RT Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.\*;

PT DNA Res. 8:11-22(2001)

DR ENBL; AF02567; BAB38411.1; -.

KW Hypothetical protein.

SQ SEQUENCE 186 AA; 21454 MW; CSEDEL66BCA9989 CRC64;

Query Match 46.8%; Score 44.5; DB 16; Length 186;

Best Local Similarity 57.1%; Pred. No. 6.6;

Matches 8; Conservative 2; Mismatches 3; Indels 1; Gaps 1

Oy 2 LRCMLGRVPRPCQ 15  
| : | : | : | : |  
Db 159 LECILNR-YKPMQ 171

RESULT 9

ID DBX3R4 PRELIMINARY; PRT: 154 AA.

AC DBX3R4

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE 4933439J1IRIK protein.

GN Mus musculus (Mouse).

OS Mus musculus; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI\_TaxID=10090;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=TESTIS;

RX MEDLINE=N1085660; PubMed=11217651;

RA Kawai J., Shimagawa A., Shibata Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Kondo S., Yamanka I., Aizawa K., Izawa M., Nishikawa H., Kasukawa T., Salto R., Saito T., Ozaki Y., Gojobori T., Pono H., Kasukawa T., Salto R., Kadota K., Matsuda H.A., Ashburner M., Bateman A., Casavant T., Fleischmann W., Gaasterland T., Glisic C., King B., Koehly H., Knehl P., Lewis S., Matsuo F., Nikaido I., Pesole G., Quackenbush J., Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barn G., Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hall D., Hofman M., Humé D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombearts P., Nordone P., Ring B., Ringwald M., Rodríguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,

RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection.",  
 RL Nature 409:685-690(2001).  
 DR EMBL: AK017132; BAB30609.1; -  
 DR MGI:191857; 493343901R1K.  
 SQ SEQUENCE 154 AA; 17921 MW; 9189DCAC8434C49 CRC64;

Query Match 46.3%; Score 44; DB 11; Length 154;  
 Best Local Similarity 61.5%; Pred. No. 6.7;  
 Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 1;  
 OY 4 CML-GRVYRCW 14  
 DB 127 CMLCGRVYRCW 139

RESULT 10  
 ID 076862 PRELIMINARY; PRT: 397 AA.  
 AC 076862;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DE EG:100610.2 protein.  
 GN EG:100610.2 OR CG2681.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydriidae; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ferraz C., Vidal S., Brun C., Bucheton A., Demaille J.G.;  
 RT Sequencing the distal x chromosome of Drosophila melanogaster.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RP [2]  
 RP SEQUENCE FROM N.A.  
 RA Benos P.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL023874; CA119647.1; -  
 DR Flybase: FBgn0024987; EG:100610.2.  
 DR InterPro: IPR004162; Sina.  
 DR Pfam: PF03145; Sina; 1.  
 SQ SEQUENCE 397 AA; 44818 MW; 98AA3314F8494565 CRC64;  
 OY Query Match 45.8%; Score 43.5; DB 5; Length 397;  
 Best Local Similarity 46.7%; Pred. No. 20;  
 Matches 7; Conservative 4; Mismatches 3; Indels 1; Gaps 1;  
 DB 62 MKCFGRVYRCW 76

RESULT 11  
 ID 094M4 PRELIMINARY; PRT: 414 AA.  
 AC 094M4;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DE EG:100610.2 protein.  
 GN EG:100610.2 OR CG2681.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydriidae; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; Pubmed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Calle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Fandell M.D., Zhang Q., Chen L.A.,  
 RA Branton R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikos G.L.G.,  
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,  
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Fabois B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegyan C.,  
 RA Jaisl M., Kalush F., Karpen G.H., Ke Z., Kentonson J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei T., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Maltel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclob J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Relbert K., Remington K., Sanders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Ventor E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhao M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003425; AAF45811.1; -  
 DR Flybase: FBgn0024987; EG:100610.2.  
 DR InterPro: IPR004162; Sina.  
 DR Pfam: PF03145; Sina; 1.  
 SQ SEQUENCE 414 AA; 46719 MW; 0E70A32A08B77640 CRC64;

Query Match 45.8%; Score 43.5; DB 5; Length 414;  
 Best Local Similarity 46.7%; Pred. No. 21;  
 Matches 7; Conservative 4; Mismatches 3; Indels 1; Gaps 1;  
 OY 2 LRCMLGRVYRCW 15  
 DB 79 MKCFGRVYRCW 93

RESULT 12  
 ID 095L0 PRELIMINARY; PRT: 103 AA.  
 AC 095L0;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DE Hypothetical 11.3 kDa protein.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-TESTIS;  
 RA Hashimoto K., Oada N., Hida M., Kusuda J., Tanuma R., Hirai M.,  
 RA Terao K., Sugano S.;  
 RT "Isolation of novel full-length cDNA clones from macaque testis cDNA  
 libraries.";

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RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL:AB072778; BAB9747.1; -.
KW Hypothetical protein.
SQ
SEQUENCE 103 AA; 11326 MW; D8547BDDA141195 CRC64;
Query Match 44.2%; Score 42; DB 6; Length 103;
Best Local Similarity 46.2%; Pred. No. 10;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 4 CMLGRVYRPMQOV 16
Db 52 CDGLSLNCPWRL 64

RESULT 13
P71972 PRELIMINARY; PRT; 250 AA.
ID P71972;
AC P71972;
DT 01-JUN-1998 (TREMBLrel. 05, Created)
DT 01-JUN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein RV2675C.
GN RV2675C OR MTCY441.44C OR MT3749.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., Rajandream N.A., Rogers K.,
RA Oliver S., Osborne J., Quail M.A., Rajandream N.A., Rogers K.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares K.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.
RL Nature 393:537-544(1998).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / OSHKOSH;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: STRONG IN C-TERMINAL REGION TO M.LEPAE U17642.
DR EMBL: Z60225; CAB0228.1; -.
DR EMBL: AEO07105; AAK47064.1; -.
DR TIGR: MT2749; -.
DR TubercuList: RV2675C; -.
DR InterPro: IPR000051; SAM_bind.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 250 AA; 27545 MW; 2EC9718C7550F32C CRC64;

Query Match 44.2%; Score 42; DB 16; Length 250;
Best Local Similarity 33.3%; Pred. No. 23;
Matches 9; Conservative 4; Mismatches 2; Indels 12; Gaps 1;

OY 2 LRCML-----GRVYRPMQOV 16
Db 218 VRCVLEFRRAIKPMLVGGRVHAPFMEV 244

RESULT 14
O9GS12

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ID O9GS12 PRELIMINARY; PRT; 311 AA.
AC O9GS12;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE F56H6.13 protein.
GN F56H6.13.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1];
RP SEQUENCE FROM N.A.
RA Kershaw J.K.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2];
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL: Z81553; CAC14333.1; -.
SQ SEQUENCE 311 AA; 36614 MW; 4A9360CE41C1027B CRC64;

Query Match 44.2%; Score 42; DB 5; Length 311;
Best Local Similarity 33.3%; Pred. No. 29;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 2 LRCMLGRVYRPMQOV 16
Db 155 MRCVVERIYNGIMWNI 169

RESULT 15
O91HR4 PRELIMINARY; PRT; 555 AA.
ID O91HR4;
AC O91HR4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Glycoprotein E (Fragment).
OS Pseudorabies virus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10345;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=GUANGDONG;
RA Lou G.M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF403050; AAK95640.1; -.
DR InterPro: IPR003404; Herpes_glycopE.
DR pfam: PF02480; Herpes_gE; 1.
FT NON_TER 555 555
FT NON_TER 1 1
SQ SEQUENCE 555 AA; 59871 MW; 79CBEF2F03003CDB CRC64;

Query Match 44.2%; Score 42; DB 12; Length 555;
Best Local Similarity 63.6%; Pred. No. 50;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 RCMILGRVYRPMQOV 13
Db 252 RCLILYVIEIPC 262

Search completed: June 25, 2003, 11:54:02
Job time : 40.04 secs

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